

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 00:02:20 ; Search time 3456 Seconds  
(without alignments)  
10047.200 Million cell updates/sec

Title: US-09-698-781-2  
Perfect score: 2144  
Sequence: 1 tgaatgaacaatactcatc.....gaaaaaaaaaaaaaaaaa 2144

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmou:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	583.8	27.2	587	14	BM993763 UI-H-DF1-
2	541.8	25.3	547	9	AL703262 DKFP686K
C 3	516.4	24.1	518	12	BF446166 BP446166
C 4	487.4	22.7	516	9	AA523498 n167h04.s
C 5	485.8	22.7	489	10	AA468294 h635f04.x
C 6	483.4	22.5	485	10	BB673586 7d39g01.x

Result No.	Score	Query Match	Length	DB ID	Description
C 7	469.8	21.9	485	12	BE855975
8	463	21.6	1108	13	BM552843
9	459	21.4	1037	13	BM554122
C 10	455.6	21.3	483	9	AT791464
11	453.6	21.2	462	12	BF897377
C 12	450.2	21.0	455	9	AT791346
13	449.2	21.0	457	9	AA885547
14	448.4	20.9	450	12	BF897404
15	444.6	20.7	1063	13	BM555970
C 16	442.2	20.6	464	12	BF897412
17	442	20.6	464	12	BF897410
C 18	438.4	20.4	461	9	AT732509
C 19	436.2	20.3	443	12	BF897401
20	429.6	20.0	445	9	AA888237
C 21	422.8	19.7	428	9	AA886557
22	422.4	19.7	803	13	BI826346
C 23	421.8	19.7	781	13	BI829771
24	421.4	19.7	808	13	BI826697
C 25	420.6	19.6	427	9	AT400952
26	418.6	19.5	454	12	BF897378
C 27	418.4	19.5	420	12	BF897376
28	406.4	19.0	419	10	AW236196
C 29	398.6	18.6	784	13	BI825564
C 30	398	18.6	406	12	BF897379
C 31	397.4	18.5	413	9	AT732549
32	397.4	18.5	419	9	AT791304
C 33	397.4	18.5	439	9	AT791506
C 34	389.8	18.2	393	9	AA522856
35	387.8	18.1	864	13	BI605544
36	386.6	18.0	728	13	BI827352
C 37	386.2	18.0	392	9	AA522850
38	378.4	17.6	904	13	BI830749
C 39	378.4	17.6	806	13	BI826010
40	374.6	17.5	760	12	BG722432
C 41	373.8	17.4	801	12	BF897366
42	371	17.3	401	13	BI831850
C 43	370.8	17.3	417	9	AA876668
44	369.4	17.2	742	12	BG722701
C 45	368.8	17.2	372	9	AA877068

## ALIGNMENTS

RESULT 1  
LOCUS BM993763/C  
DEFINITION UI-H-DF1-eug-b-15-0-UI-s1 NCI-CGAP-DF1 Homo sapiens CDNA clone  
IMAGE:5868974.3', mRNA sequence.  
ACCESSION BM993763  
VERSION BM993763.1 GI:19715416  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 587)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jose Mercende  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov  
The following repetitive elements were found in this CDNA  
sequence: 28-581>LIMC3#LINE/L1 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

## FEATURES

Location/Qualifiers  
1. 587

Source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5868974"  
/clone.lib="NCI\_CGAP\_DPL"  
/tissue.type="Subchondral Bone"  
/dev.stage="Adult"  
/lab.host="DH10B (Life Technologies)"  
/note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_DPL is a normalized cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.  
TAG\_LIB=UI-H-DPL  
TAG\_TISSUE=Subchondral bone  
TAG\_SEQ=GTTAAGCGTC"  
BASE COUNT 150 a 113 c 87 g 237 t  
ORIGIN

## Query Match

Best Local Similarity 99.7%; Pred. No. 3.3e-81;  
Matches 585; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1557 GAGTGGAGTATGAAAGGAAACATAGTACTTACAGGGGAGAAATGACAAATGACG 1616  
587 GAGTGGAGTATGAAAGGAAACATAGTACTTACAGGGGAGAAATGACAAATGACG 528  
1617 TCTTACCAAGATCAAAATTAAGCTACACAGTAAAGTCAATTCAGATTGTTCTAGA 1676  
527 TCTTACCAAGATCAAAATTAAGCTACACAGTAAAGTCAATTCAGATTGTTCTAGA 468  
1677 TAATCTTTCTAAATAATTCATATCCCAATCTAATATGAGCTAAATCCAGCAACAC 1736  
467 TAATCTTTCTAAATAATTCATATCCCAATCTAATATGAGCTAAATCCAGCAACAC 408  
1737 AAGTTGAAGGACATCTACAAATATCCCTGGGGATTTTAAAGTATTCCTCAAACTGT 1796  
407 AAGTTGAAGGACATCTACAAATATCCCTGGGGATTTTAAAGTATTCCTCAAACTGT 348  
1797 AAAAAATCATGAAATTAAGGGAATCCTGAGAAACATCAGACACATGAGACTAAGA 1856  
347 AAAAAATCATGAAATTAAGGGAATCCTGAGAAACATCAGACACATGAGACTAAGA 288  
1857 GACATGTGAGCAATGCAATGCTGCTTGTGATCAGATCCGGAACAGAAAAAGTCCAG 1916  
287 GACATGTGAGCAATGCAATGCTGCTTGTGATCAGATCCGGAACAGAAAAAGTCCAG 228  
1917 TAATGAAAAAACTGATGAAGTCTGAATGAATCTGAGATTTTAAACAGTAGTTGAT 1976  
227 TAATGAAAAAACTGATGAAGTCTGAATGAATCTGAGATTTTAAACAGTAGTTGAT 168  
1977 TTCTTAATCTTGACAAATATAGCAGGTAATTAAGATGATTAACGTTAGAGAACTGAAA 2036  
167 TTCTTAATCTTGACAAATATAGCAGGTAATTAAGATGATTAACGTTAGAGAACTGAAA 108  
2037 CTGGGTGAGGCTATCTAGGAATCTCTGTACTATCTTACCAATTTTGGGTAAGCTAA 2096  
107 CTGGGTGAGGCTATCTAGGAATCTCTGTACTATCTTACCAATTTTGGGTAAGCTAA 48  
2097 GAAACCAATGCATAAATTAAGATCTTGAATAAAAAAAAAAAAAAAAAAAAAA 2143  
47 GAAACCAATGCATAAATTAAGATCTTGAATAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 2

AL703262

LOCUS

547 bp mRNA linear EST 22-MAR-2002

DEFINITION

DKFZp666K1819.1 686 (synonym: hlc3) Homo sapiens cDNA clone

DKEP666K1819.5', mRNA sequence.

ACCESSION

AL703262.1 GI:19686617

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 547)

Poustka, A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann, S.)

EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann

, S.)

JOURNAL

Unpublished (1999)

Contact: Poustka A.J.

Department Leinrach

Max-Planck-Institute for Molecular Genetics

Innestrasse 73, 14195 Berlin, Germany

Tel: +49-30-84131623

Fax: +49-30-84131128

Email: poustka@mpg-berlin-dahlem.mpg.de

This is the 5' sequence of the clone insert

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by DKFZ (German Cancer Research Center,

Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No sl sequence available.

This clone (DKFZp666K1819) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

## FEATURES

source

1. 547

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="DKFZp666K1819"

/clone.lib="686 (synonym: hlc3)"

/tissue.type="human skeletal muscle"

/dev.stage="adult"

/lab.host="DH10B"

/note="Vector: p773-Pac; Site\_1: SfiI; Site\_2: SfiIb;

cDNA-collection"

BASE COUNT 170 a 120 c 120 g 137 t

ORIGIN

## Query Match

Best Local Similarity 99.6%; Pred. No. 1.1e-74;  
Matches 543; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GATGAAACAAATCTTCACTGCTGCTGGAACACACGTAATGACATTTTCCAGTGT 61  
3 GATGAAACAAATCTTCACTGCTGCTGGAACACACGTAATGACATTTTCCAGTGT 62  
62 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121  
63 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122  
122 TTTTACTGCTTTGTTAACCCCAACACAACTGCAAGAGAGATTGTAATACACAA 181  
123 TTTTACTGCTTTGTTAACCCCAACACAACTGCAAGAGAGATTGTAATACACAA 182  
182 TGAATGAGAGAGAGATATCTCCCTGCGCAACATGCTGGAAGATGGAATGGAACA 241  
183 TGAATGAGAGAGAGATATCTCCCTGCGCAACATGCTGGAAGATGGAATGGAACA 242  
242 AGAGGCTGAGCAATGCGCAAAAGTGGGCAAAACAGTGCATTTACAGACAGTAACC 301  
243 AGAGGCTGAGCAATGCGCAAAAGTGGGCAAAACAGTGCATTTACAGACAGTAACC 302

QY 302 AAGGATCGAATGACAACTGTAATATGTGTGAGATCTACATGTCAGTCCCGCAG 361  
DB 303 AAGGATCGAATGACAACTGTAATATGTGTGAGATCTACATGTCAGTCCCGCAG 362  
QY 362 CTCATGTCACACAGCAATCCAAAGCTGTTGATGAGTACATGATTTTGACTTGGTGT 421  
DB 363 CTCATGTCACACAGCAATCCAAAGCTGTTGATGAGTACATGATTTTGACTTGGTGT 422  
QY 422 AGGGCCAAAGACTCCCAACGAGTGTGACATATACAGTGTGTTGGTACTCTTC 481  
DB 423 AGGGCCAAAGACTCCCAACGAGTGTGACATATACAGTGTGTTGGTACTCTTC 482  
QY 482 ATACCTGCTGGATGTAATGCTACTGCTCCCAATCAAAAAGTTCTAAATACTACTA 541  
DB 483 ATACCTGCTGGATGTAATGCTACTGCTCCCAATCAAAAAGTTCTAAATACTACTA 542  
QY 542 TGTGT 546  
DB 543 TGTGT 547

RESULT 3  
BF46166/c 518 bp mRNA linear EST 01-DEC-2000  
LOCUS 7p33c05.x1 NCI\_CGAP\_P128 Homo sapiens cDNA clone IMAGE:3647601 3',  
DEFINITION mRNA sequence.  
ACCESSION BF46166  
VERSION BF46166.1 GI:11511304  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 518)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-ri@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov

Seq primer: -400p from Glibco  
High quality sequence stop: 465.

## FEATURES

Location/Qualifiers

1..518

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="3647601"

/clone\_lib="NCI\_CGAP\_P128"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI\_CGAP\_P128 was prepared, and s  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonids  
983608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

141 a 96 c 82 g 199 t

## ORIGIN

Query Match 24.1%; Score 516.4; DB 12; Length 518;  
Best Local Similarity 99.8%; Pred. No. 9.6e-71;

Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1613 GACGCTTCACCAAGTGCATAAATTAACGTACACAGTATAGCATTCAGATTGTTC 1672  
DB 518 GACGCTTCACCAAGTGCATAAATTAACGTACACAGTATAGCATTCAGATTGTTC 459  
QY 1673 TAGATAATCTTTCTAAATTCATATCCCAATCTAATATAGGTAAACATCCAGCA 1732  
DB 458 TAGATAATCTTTCTAAATTCATATCCCAATCTAATATAGGTAAACATCCAGCA 399  
QY 1733 ACTCAAGTTGAAGACATTTCTCAAAATATCCCTGGGATTTTACAGTATTCCTCA 1792  
DB 398 ACTCAAGTTGAAGACATTTCTCAAAATATCCCTGGGATTTTACAGTATTCCTCA 339  
QY 1793 CTGTAAATATCATGGAATAATAGGAATCCGTGGAACATCACAGCAGATGAGACT 1852  
DB 338 CTGTAAATATCATGGAATAATAGGAATCCGTGGAACATCACAGCAGATGAGACT 279  
QY 1853 AGAGACATGTGAGCCAAATGCAATGTGCTTCTGATCAGATCCTGGAACAGAAAA 1912  
DB 278 AGAGACATGTGAGCCAAATGCAATGTGCTTCTGATCAGATCCTGGAACAGAAAA 219  
QY 1913 TCAGTAATGAAAAAATCTGATGAGTCTGAATGATCTGAGTATTTTACAGTAGT 1972  
DB 218 TCAGTAATGAAAAAATCTGATGAGTCTGAATGATCTGAGTATTTTACAGTAGT 159  
QY 1973 TCATTTCTTATCTTGACAAATATAGCAGGTAATGATGATGATGATGATGATG 2032  
DB 158 TCATTTCTTATCTTGACAAATATAGCAGGTAATGATGATGATGATGATGATG 99  
QY 2033 GAACTGGGTGAGGCTATCTAGAAATCTCTGATCTATCTTACCAATTTTGGTAG 2092  
DB 98 GAACTGGGTGAGGCTATCTAGAAATCTCTGATCTATCTTACCAATTTTGGTAG 39  
QY 2093 CTAAGAACCATGCAAAATTAAGTACTTGAAAA 2110  
DB 38 CTAAGAACCATGCAAAATTAAGTACTTGAAAA 1

## RESULT 4

AA523498/c

LOCUS

n167h04.s1

DEFINITION

sequence.

ACCESSION

AA523498

VERSION

AA523498.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 516)

REFERENCE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-ri@mail.nih.gov  
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,  
Rodrigo F. Chuang, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert Length: 505 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 395.

## FEATURES

Location/Qualifiers

1..516

/organism="Homo sapiens"

/db\_xref="taxon:9606"

```

/clone="IMAGE:981943"
/clone.lib="NCI_CGAP_Pr12"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/notes="Vector: PAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dt priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Kitzman,
NIH."
BASE COUNT      135 a      98 c      81 g      202 t
ORIGIN

```

```

Query Match      22.7%; Score 487.4; DB 9; Length 516;
Best Local Similarity 98.6%; Pred. No. 3e-66;
Matches 502; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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OY 1635 AATTACGTCACCA-GTGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATT 1693
DB 516 AATTACGTCACCGAGGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATT 457
OY 1694 CATATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAGGACATTC 1753
DB 456 CATATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAGGACATTC 397
OY 1754 ACAAAATATCCCTGGGCTATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 1813
DB 396 ACAAAATATCCCTGGGCTATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 337
OY 1814 AGGAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCAAAATG 1873
DB 336 AGGAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCAAAATG 277
OY 1874 CAATGTGTTCTTGATAGATCTCTGGAACAGAAAAAGATCATGATGAAAAACTGATG 1933
DB 276 CAATGTGTTCTTGATAGATCTCTGGAACAGAAAAAGATCATGATGAAAAACTGATG 217
OY 1934 AAGTCGATAGATCTGAGATATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 1993
DB 216 AAGTCGATAGATCTGAGATATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 157
OY 1994 TATAGCAGGATATGATAGATGATAGAGAACTGAAACTGGGTGAGGCTATCT 2053
DB 156 TATAGCAGGATATGATAGATGATAGAGAACTGAAACTGGGTGAGGCTATCT 97
OY 2054 AGGAATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACATGCAAAATA 2113
DB 96 AGGAATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACATGCAAAATC 37
OY 2114 AAAAGTATCTGAAAAAATTTTAAAAA 2142
DB 36 CGAGTGTCTTGAATAAAAAAAAAAAAAA 8

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RESULT 5
AM468294/c 489 bp mRNA linear EST 24-FEB-2000
LOCUS he35f04.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921023 3'
DEFINITION mRNA sequence.
ACCESSION AM468294
VERSION AM468294.1 GI:7038400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov

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FEATURES
SOURCE
1. 489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2921023"
/clone.lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab_host="DH10B"
/notes="Organ: whole blood; Vector: pCMV-Sport6; Site: 1;
Salt: Site 2; Note: Cloned unidirectionally. Primer:
Oligo dt. Library constructed by Life Technologies."
BASE COUNT      136 a      92 c      77 g      184 t
ORIGIN

```

```

Query Match      22.7%; Score 485.8; DB 10; Length 489;
Best Local Similarity 99.6%; Pred. No. 5.4e-66;
Matches 487; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1637 TTACGTCACGATGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATCAT 1696
DB 489 TTACGTCACGATGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATCAT 430
OY 1697 AATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAGGACATTC 1756
DB 429 AATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAGGACATTC 370
OY 1757 AAATATCCCTGGGCTATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 1816
DB 369 AAATATCCCTGGGCTATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 310
OY 1817 GAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCAAAATG 1876
DB 309 GAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCAAAATG 250
OY 1877 TGTCCTCTTGATAGATCTCTGGAACAGAAAAAGATCATGATGAAAAACTGATG 1936
DB 249 TGTCCTCTTGATAGATCTCTGGAACAGAAAAAGATCATGATGAAAAACTGATG 190
OY 1937 TCTGAATAGATCTGAGATATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 1996
DB 189 TCTGAATAGATCTGAGATATTTTAAAGTATTCCTCAAACTGTAAATCATGAAATA 130
OY 1997 AGCAGGATATGATAGATGATAGAGAACTGAAACTGGGTGAGGCTATCTAGG 2056
DB 129 AGCAGGATATGATAGATGATAGAGAACTGAAACTGGGTGAGGCTATCTAGG 70
OY 2057 AATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACATGCAAAATA 2116
DB 69 AATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACATGCAAAATA 10
OY 2117 AGTATCTTG 2125
DB 9 AGTGTCTTG 1

```

```

RESULT 6
BE673586/c 485 bp mRNA linear EST 08-SEP-2000
LOCUS 7d39g01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3249848 3'
DEFINITION mRNA sequence.
ACCESSION BE673586

```



QY	1767	GGGGATTATTTAGAGTATTCCTCAAAACSTATAAAATCATGGAATAATGAAGGAATCCTGAG	1826
Db	365	GGGGATTATTTAGAGTATTCCTCAAAACSTATAAAATCATGGAATAATGAAGGAATCCTGAG	306
QY	1827	AAACAATCACAGACACATGAGACTAAGAGACATGTGAGCCAAATGCATGTGCTTCT	1886
Db	305	AAACAATCACAGACACATGAGACTAAGAGACATGTGAGCCAAATGCATGTGCTTCT	246
QY	1887	GGAT-CAGATCCTGGAAACGAAAAAGATTCAGTAATGAAAAAACTGATGAGTCTGATAG	1945
Db	245	GGATCGGATCCTGGAAACGAAAAAGATTCAGTAATGAAAAAACTGATGAGTCTGATAG	186
QY	1946	AATCTGGAGTATTTTAAACAGTAGTGTGATTTCTTAATCTTGACAAAATATGACAGGGTA	2005
Db	185	AATCTGGAGTATTTTAAACAGTAGTGTGATTTCTTAATCTTGACAAAATATGACAGGGTA	126
QY	2006	ATGTAAAGATGATTAACGTTAGAGAAACTGAACTGGGTGAGGGCTATCTAGAAATTCCTG	2065
Db	125	ATGTAAAGATGATTAACGTTAGAGAAACTGAACTGGGTGAGGGCTATCTAGAAATTCCTG	66
QY	2066	TACTATCTTACCAATTTTCGGTAGTCTCAAAACCAATGCAAAATATAAAAGTATCTTG	2125
Db	65	TACTATCTTACCAATTTTCGGTAGTCTCAAAACCAATGCAAAATATAAAAGTATCTTG	6
QY	2126	AAAAA 2130	
Db	5	AAAAA 1	
RESULT 8			
LOCUS	BM552843		
DEFINITION	BM552843	1108 bp	mrna
ACCESSION	AGNCOCURT_6542520	NIH_MGC_119	Homo sapiens
VERSION	BM552843		cdna clone
KEYWORDS	BM552843.1	GI:18791053	EST 20-FEB-2002
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1108)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.jnl.joy		
	plate: LLM12761	row: d	column: 14
FEATURES	High quality sequence	row: 700.	
SOURCE	location/Qualifiers		
	1. 1108		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5742685"		
	/clone_id="NIH_MGC_119"		
	/tissue_type="medulla"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: PCMV-SPORT6; Site:1: NotI;		
	Site:2: EcoRV (destroyed); RNA source normal medulla from		
	anonymous male age 27. Library is oligo-dt primed and		
	directionally cloned (EcoRV site is destroyed upon		
	cloning). Average insert size 1.3 kb, insert size range		
	0.9-3 kb. Library is normalized and enriched for		
	full-length clones and was constructed by C. Gruber		
	(Invitrogen). Research Genetics tracking code 013. Note:		

[illegible]

SOURCE ORGANISM

Homo sapiens  
human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1037)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1993)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: rgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.lnl.gov>  
Plate: LHAM12760 row: f column: 19  
High quality sequence stop: 585.  
Location/Qualifiers

FEATURES Source

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    /clone="IMAGE:5742354"  
    /clone\_1id="NIH\_MGC\_119"  
    /tissue\_type="medulla"  
    /lab\_host="DH10B"  
    /note="Organ: brain; Vector: PCMV-SPOUT6; Site\_1: NotI; site\_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH/MGC Library."  
BASE COUNT     318 a       223 c       228 g       266 t           2 others  
ORIGIN

Query Match                  21.4%   Score 459; DB 13; Length 1037;  
Best Local Similarity       76.6%; Pred. No. 5.4e-62;  
Matches 602; Conservative   0; Mismatches 176; Indels 8; Gaps 3;

OY   1 TGAATAACAATTAAGCTTCACCTCGCTGGAACCA---CTCAGATGACATTATCCCA 56  
DB   151 TAATAAGTAGAATTTTCATCTCGTGCAAAAACAATTTCCAGCATGGCTTACTRA 210  
OY   57 GTGTGTGTCTCTGCTGCTGGGCTGCCATCTTTCCAGCAAATGAAATAGAATAGAT 116  
DB   211 CGGGGGTGTCTGTGATCTGTGCTGCTCATCTTTACGTCA--GAGGAAAGGAT 267  
OY   117 CCCGGTTTTACTGTTTTGTTAACCAACCACAAACAAAGTCAAGGAGATGTGAATAAG 176  
DB   268 CCCGGTTTTACTGCTTTGTTAACCAACCAGTGTCAAGTCAAGGAGATGTGAATAAA 327  
OY   177 CACAAATGAAGTAGAGAGACAGTATCTCCCCCTGCCAGAAACATGCTGAGATGGAATGG 236  
DB   328 CACAAATGAAGTAGAGAGAGACAGTATCTCCCACCTGCCAAATGAATGCTGAAGTAGATG 387  
OY   237 AAAAAAGAGGTGCACAAATGCCAAAAGTGGGCAAAACCATGCAATTACAGCACAT 296  
DB   388 AACAGAGAGTAGAACCAAGATGCCCAAGAGTGGGCAAAACAGTGCCTTTACAAACCTAAT 447  
OY   297 AACCCAAGATGCAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTGC 356  
DB   448 GATCCAGAGAGACCGCAAAACAGTACAAATGTGTGGAATATCTCATATGTCAAGTGC 507  
OY   357 CCAGCTCATGTGCACAAAGCATCCAAAGCTGGTTGATGATGATACAAATGTTGACTTT 416  
DB   508 CTACTTCTCTGCTCTCTCAATCCAAAGCTGGTATGAGAGATCTCAATTTTGTGCTAT 567  
OY   417 GGTTGAGGGCAAAAGCTCCCAAGCAGAGTGGTTGACATTATACAGAGTTGTTGGTAC 476

Dd		568	GGTGAGACCAACAAGAATGCCAATTGCAGTTTGGACTATTAATACTCAGCTTGTTGGTAG	627
Oy	477	TCTTCATACCCTCGTTGGATGTGGAAATGCCCTACTGTCCCAATCAAANAAGTCTAAAATAC	536	
Dd	628	TGCGACTTCACGGAAGGCTGTGGAAATGCCCTACTGTCCCAATCAAANAGTCTAAAATAC	687	
Oy	537	TACATGTTTTCCAATATGTTCCTGCTGGTAAATGGGCTAATAGCATATATATGTCCTCTAT	596	
Dd	668	TACTATGTTTSCAATATGTTCCTGCTGGTAAATGGGCTAATAGCATATATATGTCCTCTAT	747	
Oy	597	GAACAAG-AGCACCTTGTGCCAGTGTGCCAGATPACTGTACAGCATGAGCATATGCACCA	655	
Dd	748	CACACGSAACACCTTGTGCCAGTGTGCCAGATPACTGTACAGCATGAGCATATGCACCA	807.	
Oy	656	TGCTTGAAGTACGAAGATCTCTATAGTAACTGTAAAAAGTTGAAGCTCACAATTAACCTG	715	
Dd	808	TAGTGTCCAGTATCAAGATCTCTCTAACGTAAGTCTGTGTAAGAAATACAGCTGGCTG	867	
Oy	716	TAAACATAGTGTGTCAGGACAGTGTGAAGCAATCCGCAATGTTGTAACAGCATTTA	775	
Dd	868	TGAACATAGTGTACTCAAGAAAGGCAAGGCTACTTGTCTATGTGCACGAATAATT	927	
Oy	776	TTAAT 781		
Dd	928	CTGAT 933		
RESULT 10	A1791464	483 bp mRNA linear EST 13-DEC-1999 AI791464		
LOCUS	n172d09.y5 NCI-CGAP_Pri12 Homo sapiens CDNA clone IMAGE:982385,			
DEFINITION	sequence.			
ACCESSION	A1791464			
VERSION	A1791464.1 GI:5339180			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
TITLE	Tumor Gene Index			
JOURNAL	Unpublished (1997)			
COMMENT	Other_ESTS: n172d09.s1 Contact: Robert Strausberg, Ph.D. Email: cgaaps@mail.nih.gov Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Dursy, M.D., Rodrigo F. Chuang, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Kitzman, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E Consortium/LNL at: <a href="http://www.bio.lnl.gov/dbip/image/Image.html">www.bio.lnl.gov/dbip/image/Image.html</a>			
FEATURES	This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: see original entry for original citation information This 5' resequenced clone has no previous 5' data to verify this new read against Putative full length read The vector to vector length is 536 Insert Length: 612 Std Error: 0.00 Seq primer: -40RP from Gibco High quality sequence stop: 445. Location/Qualifiers 1..483 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image=982385" /clone_lib="NCI_CGAP_Pri12" /sex="male"			

BASE COUNT	178 a	82 c	89 g	134 t
ORIGIN	<p> //tissue_type="metastatic prostate bone lesion"  /lab_host="DH10B"  /note="Vector: pAMP10; mRNA made from metastatic prostate  lesion of the bone, cDNA made by oligo-dT priming.  Non-directionally cloned. Size selected on agarose gel,  average insert size 600 bp. Library made by D. Kitzman,  NIH." </p>			

Query Match	21.38;	Score 455.6;	DB 9;	Length 483;
Best Local Similarity	97.18;	Pred. No. 2.6e-61;		
Matches 464; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

Qy	1607	ACAATACGCTCTTCCCAAGGATCATAAATTAAGCTACAGGTATTAAGTATTCACAT	1666
Db	6	ACTACTAAATTCGCGGCGCGCTGCACAAATTAAGCTCCAGTATTAAGTATTCACAT	65
Qy	1667	TGTGTCAGATTAATCTTTCTCAAAATATTCATATCCCAATCTAATTATGAGGCTAAACATC	1726
Db	66	TGTGTCAGATTAATCTTTCTCAAAATATTCATATCCCAATCTAATTATGAGGCTAAACATC	125
Qy	1727	CAGCAATCTCAAGTGAAGACATTTCTCAAAATATATCCCTGGGCTATTTAGAGATATCC	1786
Db	126	CAGCAATCTCAAGTGAAGACATTTCTCAAAATATATCCCTGGGCTATTTAGAGATATTC	185

Qy 1787 TCAAACGTAATAATCATGGAAATTAAGGGAATCCTGAGAAACAATCACAGACCACATG 1846  
|||||  
Db 186 TCAAACGTAATAATCATGGAAATTAAGGGAATCCTGAGAAACAATCACAGACCACATG 245

104 / AGAC TAAAGGAGACATG TGGCCCAATG CAAATG TCGCTCTT TGGATC CAATC CCGGAACAGA 1906  
 |||||  
 246 AGACTAAGGAGACATGTGAGCCAAATGCATGTGCTCTTGGATCAATCCCGGAACAGA 305

306 AAAAGATCAGTAATGAAAACTGATGAGCTCTGATAGAACTCTGGAGTATTTTAAACAG 365

Db 366 TACTGTCATTCTTAATCTTGACAAATATAGCAGGTAATGATGATTAACGTTAGA 425

Db 426 GAACTGAACCTGGGTGAGGGCTACTAGSATTCTCTGACTATCTTACCAATTTT 483

	LOCUS	DEFINITION	FEATURES	EST ID
RESULT 11	BF897377/C			
LOCUS	BF897377	462 bp	mRNA linear	EST_18-JAN-2001
DEFINITION	IL2-MT0181-281100-265-A05 MT0181	Homo sapiens CDNA	mRNA sequence	

ACCESSION	BF09/3//	GI:12288836
VERSION	BF0897377.1	
KEYWORDS	EST.	
SOURCE	human.	

REFERENCE  
1 (bases 1 to 462)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D. Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hara

TITLE	Author	Journal	Year	Volume	Page	DOI
Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Simpson, A.J.	Proc Natl Acad Sci U S A	2003	100	12073-12078	10.1073/pnas.12073-12078

**JOURNAL MEDLINE COMMENT**  
 Price: Medl. Acad. Sci. U.S.A. 9 (1), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-S

Brazil  
 Tel : +55-11-27049422  
 Fax: +55-11-3707001  
 Email: asimpson@udwig.org.br  
 This sequence was derived from the RPESP/LICR Human Cancer Genome  
 project. This entry can be seen in the following URL  
 (<http://www.udwig.org.br/scripts/gethtml2.pl?Cl=IL2&L2=IL2-MT0181>  
 281100-265-A05&L3=2000-11-28&L4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 461.  
 Location/Qualifiers  
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/clone_lib="MT0181"
/dev_stage="Adult"
/note="Organ: marrow; Vector: Puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 199
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      131 a      99 c      94 g      136 t      2 others
ORIGIN

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Query Match	21.2%	Score	453.6	DB	12	Length	462
Best Local Similarity	98.7%	Pred	No. 5.4e-61				
Matches	456	Conservative	0	Mismatches	6	Indels	0
						Gaps	0

OY 307 ATCGAATGACAGCTCTAAATGTGGTGAGAACTCTACTGTCAAGTGGCCCCAGCTCAT 366  
 |||||  
 462 ATCGAATGACCAAGTCTAAATGTGGTGAGATNCTCTACATGTCAAGTGGCCCCNCAAGTCTAT 403

	387	GCTCACAGCAATCCAAAGCGTGTGATGAGACAAATATTGTGACTTTGGTAGGGC	426
VY			
Db	402	GGTCACAAGCAATCCAAAGCGTGTGATGAGTCAATGATTGTGACTTTGGTGAGGCC	343

Db 342 CAAAGACTCACAACCTCAGTGGTTGGACATTATACACAGAGTGTGGTACTCTTCATACC 283

Db 282 TCCTTGCAATGTCGCAATSCCTACTGTCCCCAATCAAAAAGTTCTAAATACACTATGTTT 223

Db 222 GCCAATATTGCTCCTGCTGTAATGGCGCATATGACTATATGTCCTTTGACACAGAG 163

Db 162 CACCTTGTGCCAGTTGCCAGATACTGTGACGATGTGACTATGCACCAATGGTTGCACGT 103  
 667 AGCAAGATCTCTATAGTAACCTGAAAAACGCTGGAAACCTTACATATTAATCCCTTTAAATATCACT 736

DB	102	ACGAAGATCTCTATAGTAACTGTAAAAAGCTTTGAGCTCACCATTAACTGTAACCATCACT	43
QV	727	TGCTCAGGAGACAGTTGCAAGGCATCCCTGCATATGTTCAACA	768

Db 42 TGGTCAGGGACAGTTGCAAGGCCCTCCCTGCATTTGTTCAACACA 1

LOCUS	A17913346	455 bp	mRNA	linear	EST 13-DEC-1995
DEFINITION	h3030109.y5 NCI.CGAP.Pr3 Homo sapiens CDNA clone IMAGE:953921, mRNA				

ACCESSION	sequence.
VERSION	AI791346
KEYWORDS	AI791346.1 GI:5339062
SOURCE	EST.
ORGANISM	human.
	Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 453)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL  
COMMENT  
Unpublished (1997)  
Other-ESTs: nh30h09.x5

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Kitzman, Ph.D.  
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/dbp/image/image.html](http://www-bio.llnl.gov/dbp/image/image.html)

FEATURES  
SOURCE  
This read is a RESEQUENCE of a previously sequenced human clone  
Original clone citation: see original entry for original citation.  
Information  
This 5' resequenced clone has no previous 5' data to verify this  
new read against  
Putative full length read  
The vector to vector length is 502  
Insert Length: 504 Std Error: 0.00  
Seq primer: -40RP from Gibco  
High quality sequence stop: 441.  
Location/Qualifiers  
1..455

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/sex="Male"  
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/lab\_host="DH10B"  
/note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors. 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kitzman."

BASE COUNT 172 a 73 c 85 g 125 t

Query Match 21.0%; Score 450.2; DB 9; Length 455;

Best Local Similarity 99.3%; Pred. No. 1.8e-60;

Matches 452; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1627 GTCATCAAAATTTACGTCACGATGATTAAGTCAATTTGTTCTAGATAATCTTTCT 1686.

DB 1 GTCGCAAAATTTACGTCACGATGATTAAGTCAATTTGTTCTAGATAATCTTTCT 60

QY 1687 AAAAATTCATATCCCAATCTAATTTAGCTAAACATCCACCAACCAAGTGAAG 1746

DB 61 AAAAATTCATATCCCAATCTAATTTAGCTAATCAATCCACCAACCAAGTGAAG 120

QY 1747 ACATTTACAAATATATCCCTGGGATTTTAGAGTATCTCTCAAACTGTAATATCATG 1806

DB 121 ACATTTACAAATATATCCCTGGGATTTTAGAGTATCTCTCAAACTGTAATATCATG 180

QY 1807 GAAATTAAGGAATCTCTGAGAAACATCAACACGATGAGCTAAGAGACATGTGAG 1866

DB 181 GAAATTAAGGAATCTCTGAGAAACATCAACACGATGAGCTAAGAGACATGTGAG 240

QY 1867 CCAATGCAATGTCTTCTTGATGATCAGATCCTGAGACAGAAAAAGATGATAAGAAA 1926

DB 241 CCAATGCAATGTCTTCTTGATGATCAGATCCTGAGACAGAAAAAGATGATAAGAAA 300

QY 1927 ACTGATGAAGTCTGATAGATCTGGAGTATTTTAAACAGTACTGTTGATTTCTTAATCT 1986

DB 301 ACTGATGAAGTCTGATAGATCTGGAGTATTTTAAACAGTACTGTTGATTTCTTAATCT 360

QY 1987 TGACAAATATACGAGGCTAATGATATATACCTTAAGAAACGAACTGGGAGG 2046

DB 361 TGACAAATATACGAGGCTAATGATATATACCTTAAGAAACGAACTGGGAGG 420

QY 2047 GCATCTAGCAATTCCTCTACTATCTTACCAAT 2081

DB 421 GCATCTAGCAATTCCTCTACTATCTTACCAAT 455

RESULT 13  
AA885547 457 bp mRNA linear EST 30-MAR-1998  
LOCUS  
DEFINITION  
AA885547 n532ell.s1 NCI-CCAP\_Pr12 Homo sapiens cDNA clone IMAGE:1291436,  
mRNA sequence.

ACCESSION  
AA885547

VERSION  
AA885547.1 GI:3000655

KEYWORDS  
EST.

SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 457)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index  
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Durey, M.D.,  
Rodrigo F. Chuagui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Kitzman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/dbp/image/image.html](http://www-bio.llnl.gov/dbp/image/image.html)  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 421.  
Location/Qualifiers  
1..457

FEATURES  
source

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/clone="IMAGE:1291436"  
/clone\_1ib="NCI-CCAP\_Pr12"  
/sex="male"  
/issue\_type="metastatic prostate bone lesion"

/lab\_host="DH10B"

/note="Vector: PAMP10; mRNA made from metastatic prostate  
lesion of the bone. cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel,  
average insert size 600 bp. Library made by D. Kitzman,  
NIH.

BASE COUNT 176 a 74 c 88 g 119 t

ORIGIN

Query Match 21.0%; Score 449.2; DB 9; Length 457;

Best Local Similarity 99.3%; Pred. No. 2.6e-60;

Matches 451; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1601 AAAATGCAAAATGATCGCTTACCAAGTATCAAAATTAAGTCACAGTATAGATCAT 1660

DB 4 AAAATGCAAAATGATCGCTTACCAAGGATCAAAATTAAGTCACAGTATAGATCAT 63

QY 1661 TCAGATTTGTTCTAGATTAATCTTTCAAAATTCATAATCCCAATCTAATATGAGCTAA 1720

DB 64 CCAGATTTGTTCTAGATTAATCTTTCAAAATTCATAATCCCAATCTAATATGAGCTAA 123

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QY 1721 AACATCCGCAAACTCAAGTTGAAGACATTTACAAAATATCCCTGGGTATTTAGAG 1780
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Db 124 AACATCCGCAAACTCAAGTTGAAGACATTTACAAAATATCCCTGGGTATTTAGAG 183
QY 1781 TATTCCTCAAAAGCTGTAATAATCATGGAATAAGGAATCCCTGAGAAACATCACAGAC 1840
      |||||||
Db 184 TATTCCTCAAAAGCTGTAATAATCATGGAATAAGGAATCCCTGAGAAACATCACAGAC 243
QY 1841 CACATGAGACTAAGAGACATGTGAGCCAAATGCAATGTCTCTTGGATCAGATCCTGG 1900
      |||||||
Db 244 CACATGAGACTAAGAGACATGTGAGCCAAATGCAATGTCTCTTGGATCAGATCCTGG 303
QY 1901 AACAGAAAAAGATCAGTATGAAAAAACTGATGAGTGAATAGATCTGAGATATTTT 1960
      |||||||
Db 304 AACAGAAAAAGATCAGTATGAAAAAACTGATGAGTGAATAGATCTGAGATATTTT 363
QY 1961 TAACAGTAGTGTGATTTCTTATCTTGACAAATATACGCGGTATGTATGATATAC 2020
      |||||||
Db 364 TAACAGTAGTGTGATTTCTTATCTTGACAAATATACGCGGTATGTATGATATAC 423
QY 2021 GTTAGAGAAACTGAACTGGGTGAGGCTATCTA 2054
      |||||||
Db 424 GTTAGAGAAACTGAACTGGGTGAGGCTATCTA 457

RESULT 14
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DEFINITION IL2-MT0181-281100-265-E05 MT0181 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF897404
VERSION BF897404.1 GI:12288850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 450)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed
MEDLINE sequence tags
COMMENT Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
CONTACT: Simpson A.J.G.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&ct=IL2-MT0181-
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1063)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@ds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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http://image.jnl.gov
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